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FIGURE 5

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1  ATGGAACCTG AGTGCCTCGG ACATCACCCG GGTCTTCAAA CTCTACGGCT GCAGCCCAAG
   w n l s a s d i t r v l k l y g c s p

61  TGGCCCCAGG CCCCCTGGGA GAGGGTCCCA TGCCACAGC ACTGGTAGGA GCCCCGCTCC
   s g p r p r g r g s h a h s t g r s p a

121  GGCCTCCCTA TCTCTGCAGC GGCTTTTGGG GGCCTGTCTG GCGGAATCCA GGAGCCCCGA
   p a s l s l q r l l e a l s a e s r s p

181  CCCCAGTGGT TCCAGTGCGG GAGGCCAGCC CGTTCCTGCA GGGCCTGGGG AGAGCCCACA
   d p s g s s a g g q p v p a g p g e s p

241  TGGGTGGGAG TCCCCTGCCC TGAAAAAGCT CAGTGCAGAG GCCTCGGCAA GGCAGCCTCA
   h g w e s p a l k k l s a e a s a r q p

301  GACCCTAGCT TCCTCCCCAA GATCAAGGCC TGGAGCAGGT GCCCCGGGTG TTGCTCAGGA
   q t l a s s p r s r p g a g a p g v a q

361  GCAGTCCTGG CTGGCCGGAG TGTCCACCAA GCCACAGTC CCATCTTCAG AAGCAGGAAT
   e q s w l a g v s t k p t v p s s e a g

421  CCAGCCAGTC CCTGTCCAGG GAAGCCCAGC TCTGCCAGGG GGCTGTGTAC CTAGAAATCA
   i q p v p v q g s p a l p g g c v p r n

481  TTTCAAGGGG ATGTCCGAAG ATTAAGCCTG TGGCTTCTGT CCCCAGTAG GGAGGGCATC
   h f k g m s e d

541  CTCTGCCCAG TGGAGCTGGG TCGTCTACCT CTTGGCTCCT TTGGGCCACA CCACTGTCTT
601  CCAGCCCCAA CCTACCACCC CATCTCAGAG GGCCAGGACT CTTCCCCTGT CTCTCTTCAC
661  TGTGTTCCCC TAAGGGCTCC TAGGGCCAGG GGTTCCTTCTA GCTCTGCCAC AGGGGAAGGC
721  AGGCCTGGCT GTGCCTGCTC TTGACTTTTG CCCAGCCCTG GTGGATGCTG GGAATGGGAG
781  GTGACATTCT CCAGGGACAG GTCCTGGAAG GGGTGGGGAA GAGGTAGGTT CCAGCCCCGC
841  AGAACCCTGG AATCCCTCCT GTGCCTGAGG CCCTGCCCCC CAGCATGGAC TAATGGTGTC
901  CCTACCTCTC CCTCAGGGCA GCCCTGTGGC TGGGACCCTG GGAACAGCCT CCCATCCCAC
961  CCAACATGCC CAAGTGTGGG GGAATGTTCT ACAGCAGTGT AGCCTCCAGC CCTTCTCTCC
1021  AGGAGGCTTT GAGAGCCCAA CTTACTCCCC TGCAGAGCAG GAAGGTGGTA GGTCAAGTGT
1081  GGCCACCATT GGGGAGACGA GAAAGAAGTG GGGCCCCACC AGATTGCACA ATGGGAACCT
1141  CAGCTGGCCC CTGAACAGAG GACTCAGTTG TCTCCACCCT ACACCGCTAT TCCCTGGAGC
1201  TCAGCCAGGC GCAGCCTTGG AAGGAGAAAG GGCTGGGGTT ACCTGGCTTG TCCTCCTCCA
1261  GGAAAGCCCC CTTCCTCCTC TGCCCCAGCT CCCAGCCTGG CCTCCTCCAG GCAGGCCCTA
1321  CTCCTCTGCC CCAGCTCCGG CTTTCCCCAT GAGGTTTGTC CCAGGCATGA AGAAAGCATC
1381  CAGGGTGCCA ATGAGTGGGC CTAGGCCAGA GGCCCCCAG TCCCCAAGGG TACTGTTTTG
1441  GTGGCCTTTC AGAGGGTCAA GGAAGCCCTG CTTGGGGTAG AAGGGGCAGG AGCCCCACAT
1501  GTTGGGGGAG GAAATAAAGT GGAGTGTGCT GTGCTGAAAA AAAAAAAAAA AAAA

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TAA Stop codon

AATAAA Consensus polyadenylation site (underlined)

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FIGURE 10 (continued)

1081 CTCGGCAAGG CAGCCTCAGA CCCTAGCTTC CTCCCCAAGA TCAAGGCCTG GAGCAGGTGC
a s a r q p q t l a s s p r s r p g a g

1141 CCCCgGTGTT GCTCAGGAGC AGTCCTGGCT GGCCGGAGTG TCCACCAAGC CCACAGTCCC
a p g v a q e q s w l a g v s t k p t v

1201 ATCTTCAGAA GCAGGAATCC AGCCAGTCCC TGTCCAGGGA AGCCCAGCTC TGCCAGGGGG
p s s e a g i q p v p v q g s p a l p g

1261 CTGTGTACCT AGAAATCATT TCAAGGGGAT GTCCGAAGAT TAAGCCTGTG GCT
g c v p r n h f k g m s e d

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FIGURE 13

Active site residues are underlined below.

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WO2002/16566-A2      -----MEGVGGLWPWVLGLLSLPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI
AX526191              MSCCLVSPVGAPGICVCPCLSGPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI
INSP005 PREDICTION    -----
INSP005b              -----MEGVGGLWPWVLGLLSLPGVILGAPLASSCAGACGTSFPDGLTPEGTQASGDKDI
INSP005a              -----

WO2002/16566-A2      PAINQGLILEETPESSFLIEGDIIRPSPFRLLSATS NKWPMGGSGVVEVPFLLSSKYDEP
AX526191              PAINQGLILEETPESSFLIEGDIIRPSPFRLLSATS NKWPMGGSGVVEVPFLLSSKYDEP
INSP005 PREDICTION    -----WPMGGSGVVEVPFLLSSKYDEP
INSP005b              PAINQGLILEETPESSFLIEGDIIRPSPFRLLSATS NKWPMGGSGVVEVPFLLSSKYDEP
INSP005a              -----MGGSGVVEVPFLLSSKYDEP
                               *****

WO2002/16566-A2      SRQVILEALAEFERSTCIRFVTYQDQ RDFISIIPMYGCFSSVGRSGGMQVVS LAPTC LQK
AX526191              SRQVILEALAEFERSTCIRFVTYQDQ RDFISIIPMYGCFSSVGRSGGMQVVS LAPTC LQK
INSP005 PREDICTION    SHQVILEALAEFERSTCIRFVTYQDQ RDFISIIPMYGCFSSVGRSGGMQVVS LAPTC LQK
INSP005b              SRQVILEALAEFERSTCIRFVTYQDQ RDFISIIPMYGCFSSVGRSGGMQVVS LAPTC LQK
INSP005a              SRQVILEALAEFERSTCIRFVTYQDQ RDFISIIPMYGCFSSVGRSGGMQVVS LAPTC LQK
                               *:*****

WO2002/16566-A2      GRGIVLHELMHVLGFWHEHTRADRDRIYIRVNWNEILPGFEINFIKSRSSNMLTPYDYSSV
AX526191              GRGIVLHELMHVLGFWHEHTRADRDRIYIRVNWNEILPGFEINFIKSRSSNMLTPYDYSSV
INSP005 PREDICTION    GRGIVLHELMHVLGFWHEHTRADRDRIYIRVNWNEILPGFEINFIKSQSSNMLTPYDYSSV
INSP005b              GRGIVLHELMHVLGFWHEHTRADRDRIYIRVNWNEILPGFEINFIKSRSSNMLTPYDYSSV
INSP005a              GRGIVLHELMHVLGFWHEHTRADRDRIYIRVNWNEILPGFEINFIKSQSSNMLTPYDYSSV
                               *****

WO2002/16566-A2      MHYGRLAFSRRGLPTITPLWAPSVHIGQRWNLSASDITRVLKLYGCSPSGPRPRGRG---
AX526191              MHYGRLAFSRRGLPTITPLWAPSVHIGQRWNLSASDITRVLKLYGCSPSGPRPRGRGSHA
INSP005 PREDICTION    MHYGRLAFSRRGLPTITPLWAPSVHIGQRWNLSASDITRVLKLYGC-----
INSP005b              MHYGRLAFSRRGLPTITPLWAPSVHIGQRWNLSASDITRVLKLYGCSPSGPRPRGRGSHA
INSP005a              MHYGRLAFSRRGLPTITPLWAPSVHIGQRWNLSASDITRVLKLYGCSPSGPRPRGRGSHA
                               *****:.. . . .:

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WO2002/16566-A2 -----EWHG---RKVT  
AX526191 HSTGRSPAPASLSLQRLLEALSAESRSPDPGSSAGGQPVPAGPGESPHGWESPALKKLS  
INSP005 PREDICTION -----  
INSP005b HSTGRSPAPASLSLQRLLEALSAESRSPDPGSSAGGQPVPAGPGESPHGWESPALKKLS  
INSP005a HSTGRSPAPASLSLQRLLEALSAESRSPDPGSSAGGQPVPAGPGESPHGWESPALKKLS  
  
:: ::::: : . : :::: :::::::::::::::::::: ..... :.: .:  
  
WO2002/16566-A2 -----  
AX526191 AEASARQPQTlassPRSRPGAGAPGVAEQSWLAGVSTKPTVPSSEAGIQPVPVQGSPAL  
INSP005 PREDICTION -----  
INSP005b AEASARQPQTlassPRSRPGAGAPGVAEQSWLAGVSTKPTVPSSEAGIQPVPVQGSPAL  
INSP005a AEASARQPQTlassPRSRPGAGAPGVAEQSWLAGVSTKPTVPSSEAGIQPVPVQGSPAL  
  
:::~ ..: ~::: : ~:::~ ~::: :~ ~:::~ ~:::~ .. . ~:::~  
  
WO2002/16566-A2 -----  
AX526191 PGGCvPRNHFKGMSED  
INSP005 PREDICTION -----  
INSP005b PGGCvPRNHFKGMSED  
INSP005a PGGCvPRNHFKGMSED  
  
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